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Reviewer: Durreshwar Anjum

Timestamp: [year=2011; month=12; day=20; hr=11; min=36; sec=40; ms=752;
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Application No: 10584424

Version No: 2.0

Input Set:**Output Set:****Started:** 2011-12-12 13:24:59.439**Finished:** 2011-12-12 13:25:02.321**Elapsed:** 0 hr(s) 0 min(s) 2 sec(s) 882 ms**Total Warnings:** 68**Total Errors:** 0**No. of SeqIDs Defined:** 80**Actual SeqID Count:** 80

Error code	Error Description
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W 213	Artificial or Unknown found in <213> in SEQ ID (12)
W 213	Artificial or Unknown found in <213> in SEQ ID (13)
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W 213	Artificial or Unknown found in <213> in SEQ ID (28)
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Input Set:

Output Set:

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Total Warnings: 68
Total Errors: 0
No. of SeqIDs Defined: 80
Actual SeqID Count: 80

Error code

Error Description

This error has occurred more than 20 times, will not be displayed

SEQUENCE LISTING

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Sleep, Darrell
Shuttleworth, Gillian
Finnis, Christopher John Arthur

<120> Gene Expression Technique

<130> 11075.204-US

<140> 10584424

<141> 2011-12-12

<150> PCT/GB2004/005462

<151> 2004-12-23

<150> GB 0329681.1

<151> 2003-12-23

<160> 80

<170> PatentIn version 3.5

<210> 1

<211> 522

<212> PRT

<213> *Saccharomyces cerevisiae*

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35 40 45

His Asp Leu Val Leu Ala Glu Phe Phe Ala Pro Trp Cys Gly His Cys
50 55 60

Lys Asn Met Ala Pro Glu Tyr Val Lys Ala Ala Glu Thr Leu Val Glu
65 70 75 80

Lys Asn Ile Thr Leu Ala Gln Ile Asp Cys Thr Glu Asn Gln Asp Leu
85 90 95

Cys Met Glu His Asn Ile Pro Gly Phe Pro Ser Leu Lys Ile Phe Lys
100 105 110

Asn Ser Asp Val Asn Asn Ser Ile Asp Tyr Glu Gly Pro Arg Thr Ala
115 120 125

Glu Ala Ile Val Gln Phe Met Ile Lys Gln Ser Gln Pro Ala Val Ala
130 135 140

Val Val Ala Asp Leu Pro Ala Tyr Leu Ala Asn Glu Thr Phe Val Thr
145 150 155 160

Pro Val Ile Val Gln Ser Gly Lys Ile Asp Ala Asp Phe Asn Ala Thr
165 170 175

Phe Tyr Ser Met Ala Asn Lys His Phe Asn Asp Tyr Asp Phe Val Ser
180 185 190

Ala Glu Asn Ala Asp Asp Asp Phe Lys Leu Ser Ile Tyr Leu Pro Ser
195 200 205

Ala Met Asp Glu Pro Val Val Tyr Asn Gly Lys Lys Ala Asp Ile Ala
210 215 220

Asp Ala Asp Val Phe Glu Lys Trp Leu Gln Val Glu Ala Leu Pro Tyr
225 230 235 240

Phe Gly Glu Ile Asp Gly Ser Val Phe Ala Gln Tyr Val Glu Ser Gly
245 250 255

Leu Pro Leu Gly Tyr Leu Phe Tyr Asn Asp Glu Glu Glu Leu Glu Glu
260 265 270

Tyr Lys Pro Leu Phe Thr Glu Leu Ala Lys Lys Asn Arg Gly Leu Met
275 280 285

Asn Phe Val Ser Ile Asp Ala Arg Lys Phe Gly Arg His Ala Gly Asn
290 295 300

Leu Asn Met Lys Glu Gln Phe Pro Leu Phe Ala Ile His Asp Met Thr
305 310 315 320

Glu Asp Leu Lys Tyr Gly Leu Pro Gln Leu Ser Glu Glu Ala Phe Asp
325 330 335

Glu Leu Ser Asp Lys Ile Val Leu Glu Ser Lys Ala Ile Glu Ser Leu
340 345 350

Val Lys Asp Phe Leu Lys Gly Asp Ala Ser Pro Ile Val Lys Ser Gln
355 360 365

Glu Ile Phe Glu Asn Gln Asp Ser Ser Val Phe Gln Leu Val Gly Lys
370 375 380

Asn His Asp Glu Ile Val Asn Asp Pro Lys Lys Asp Val Leu Val Leu
385 390 395 400

Tyr Tyr Ala Pro Trp Cys Gly His Cys Lys Arg Leu Ala Pro Thr Tyr
405 410 415

Gln Glu Leu Ala Asp Thr Tyr Ala Asn Ala Thr Ser Asp Val Leu Ile
420 425 430

Ala Lys Leu Asp His Thr Glu Asn Asp Val Arg Gly Val Val Ile Glu
435 440 445

Gly Tyr Pro Thr Ile Val Leu Tyr Pro Gly Gly Lys Lys Ser Glu Ser
450 455 460

Val Val Tyr Gln Gly Ser Arg Ser Leu Asp Ser Leu Phe Asp Phe Ile
465 470 475 480

Lys Glu Asn Gly His Phe Asp Val Asp Gly Lys Ala Leu Tyr Glu Glu
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Ala Gln Glu Lys Ala Ala Glu Glu Ala Asp Ala Asp Ala Glu Leu Ala
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Asp Glu Glu Asp Ala Ile His Asp Glu Leu
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<212> PRT
<213> *Saccharomyces cerevisiae*

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Ala Val Val Lys Leu Ala Thr Asp Ser Phe Asn Glu Tyr Ile Gln Ser	35	40	45
His Asp Leu Val Leu Ala Glu Phe Phe Ala Pro Trp Cys Gly His Cys	50	55	60
Lys Asn Met Ala Pro Glu Tyr Val Lys Ala Ala Glu Thr Leu Val Glu	65	70	75
Lys Asn Ile Thr Leu Ala Gln Ile Asp Cys Thr Glu Asn Gln Asp Leu	85	90	95
Cys Met Glu His Asn Ile Pro Gly Phe Pro Ser Leu Lys Ile Phe Lys	100	105	110
Asn Arg Asp Val Asn Asn Ser Ile Asp Tyr Glu Gly Pro Arg Thr Ala	115	120	125
Glu Ala Ile Val Gln Phe Met Ile Lys Gln Ser Gln Pro Ala Val Ala	130	135	140
Val Val Ala Asp Leu Pro Ala Tyr Leu Ala Asn Glu Thr Phe Val Thr	145	150	155
Pro Val Ile Val Gln Ser Gly Lys Ile Asp Ala Asp Phe Asn Ala Thr	165	170	175
Phe Tyr Ser Met Ala Asn Lys His Phe Asn Asp Tyr Asp Phe Val Ser	180	185	190
Ala Glu Asn Ala Asp Asp Asp Phe Lys Leu Ser Ile Tyr Leu Pro Ser	195	200	205
Ala Met Asp Glu Pro Val Val Tyr Asn Gly Lys Lys Ala Asp Ile Ala	210	215	220
Asp Ala Asp Val Phe Glu Lys Trp Leu Gln Val Glu Ala Leu Pro Tyr	225	230	235
			240

Phe Gly Glu Ile Asp Gly Ser Val Phe Ala Gln Tyr Val Glu Ser Gly
245 250 255

Leu Pro Leu Gly Tyr Leu Phe Tyr Asn Asp Glu Glu Glu Leu Glu Glu
260 265 270

Tyr Lys Pro Leu Phe Thr Glu Leu Ala Lys Lys Asn Arg Gly Leu Met
275 280 285

Asn Phe Val Ser Ile Asp Ala Arg Lys Phe Gly Arg His Ala Gly Asn
290 295 300

Leu Asn Met Lys Glu Gln Phe Pro Leu Phe Ala Ile His Asp Met Thr
305 310 315 320

Glu Asp Leu Lys Tyr Gly Leu Pro Gln Leu Ser Glu Glu Ala Phe Asp
325 330 335

Glu Leu Ser Asp Lys Ile Val Leu Glu Ser Lys Ala Ile Glu Ser Leu
340 345 350

Val Lys Asp Phe Leu Lys Gly Asp Ala Ser Pro Ile Val Lys Ser Gln
355 360 365

Glu Ile Phe Glu Asn Gln Asp Ser Ser Val Phe Gln Leu Val Gly Lys
370 375 380

Asn His Asp Glu Ile Val Asn Asp Pro Lys Lys Asp Val Leu Val Leu
385 390 395 400

Tyr Tyr Ala Pro Trp Cys Gly His Cys Lys Arg Leu Ala Pro Thr Tyr
405 410 415

Gln Glu Leu Ala Asp Thr Tyr Ala Asn Ala Thr Ser Asp Val Leu Ile
420 425 430

Ala Lys Leu Asp His Thr Glu Asn Asp Val Arg Gly Val Val Ile Glu
435 440 445

Gly Tyr Pro Thr Ile Val Leu Tyr Pro Gly Gly Lys Lys Ser Glu Ser
450 455 460

Val Val Tyr Gln Gly Ser Arg Ser Leu Asp Ser Leu Phe Asp Phe Ile
465 470 475 480

Lys Glu Asn Gly His Phe Asp Val Asp Gly Lys Ala Leu Tyr Glu Glu
485 490 495

Ala Gln Glu Lys Ala Ala Glu Glu Ala Glu Ala Asp Ala Glu Ala Glu
500 505 510

Ala Asp Ala Asp Ala Glu Leu Ala Asp Glu Glu Asp Ala Ile His Asp
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Glu Leu
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<213> *Saccharomyces cerevisiae*

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<210> 4
<211> 642
<212> PRT
<213> *Saccharomyces cerevisiae*

<400> 4

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Asn Arg Thr Thr Pro Ser Phe Val Ala Phe Thr Asp Thr Glu Arg Leu
35 40 45

Ile Gly Asp Ala Ala Lys Asn Gln Ala Ala Met Asn Pro Ser Asn Thr
50 55 60

Val Phe Asp Ala Lys Arg Leu Ile Gly Arg Asn Phe Asn Asp Pro Glu
65 70 75 80

Val Gln Ala Asp Met Lys His Phe Pro Phe Lys Leu Ile Asp Val Asp
85 90 95

Gly Lys Pro Gln Ile Gln Val Glu Phe Lys Gly Glu Thr Lys Asn Phe
100 105 110

Thr Pro Glu Gln Ile Ser Ser Met Val Leu Gly Lys Met Lys Glu Thr
115 120 125

Ala Glu Ser Tyr Leu Gly Ala Lys Val Asn Asp Ala Val Val Thr Val
130 135 140

Pro Ala Tyr Phe Asn Asp Ser Gln Arg Gln Ala Thr Lys Asp Ala Gly
145 150 155 160

Thr Ile Ala Gly Leu Asn Val Leu Arg Ile Ile Asn Glu Pro Thr Ala
165 170 175

Ala Ala Ile Ala Tyr Gly Leu Asp Lys Lys Gly Lys Glu Glu His Val
180 185 190

Leu Ile Phe Asp Leu Gly Gly Gly Thr Phe Asp Val Ser Leu Leu Phe
195 200 205

Ile Glu Asp Gly Ile Phe Glu Val Lys Ala Thr Ala Gly Asp Thr His
210 215 220

Leu Gly Gly Glu Asp Phe Asp Asn Arg Leu Val Asn His Phe Ile Gln
225 230 235 240

Glu Phe Lys Arg Lys Asn Lys Lys Asp Leu Ser Thr Asn Gln Arg Ala
245 250 255

Leu Arg Arg Leu Arg Thr Ala Cys Glu Arg Ala Lys Arg Thr Leu Ser
260 265 270

Ser Ser Ala Gln Thr Ser Val Glu Ile Asp Ser Leu Phe Glu Gly Ile
275 280 285

Asp Phe Tyr Thr Ser Ile Thr Arg Ala Arg Phe Glu Glu Leu Cys Ala
290 295 300

Asp Leu Phe Arg Ser Thr Leu Asp Pro Val Glu Lys Val Leu Arg Asp			
305	310	315	320
Ala Lys Leu Asp Lys Ser Gln Val Asp Glu Ile Val Leu Val Gly Gly			
	325	330	335
Ser Thr Arg Ile Pro Lys Val Gln Lys Leu Val Thr Asp Tyr Phe Asn			
	340	345	350
Gly Lys Glu Pro Asn Arg Ser Ile Asn Pro Asp Glu Ala Val Ala Tyr			
	355	360	365
Gly Ala Ala Val Gln Ala Ala Ile Leu Thr Gly Asp Glu Ser Ser Lys			
	370	375	380
Thr Gln Asp Leu Leu Leu Leu Asp Val Ala Pro Leu Ser Leu Gly Ile			
385	390	395	400
Glu Thr Ala Gly Gly Val Met Thr Lys Leu Ile Pro Arg Asn Ser Thr			
	405	410	415
Ile Ser Thr Lys Lys Phe Glu Ile Phe Ser Thr Tyr Ala Asp Asn Gln			
	420	425	430
Pro Gly Val Leu Ile Gln Val Phe Glu Gly Glu Arg Ala Lys Thr Lys			
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Asp Asn Asn Leu Leu Gly Lys Phe Glu Leu Ser Gly Ile Pro Pro Ala			
450	455	460	
Pro Arg Gly Val Pro Gln Ile Glu Val Thr Phe Asp Val Asp Ser Asn			
465	470	475	480
Gly Ile Leu Asn Val Ser Ala Val Glu Lys Gly Thr Gly Lys Ser Asn			
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Lys Ile Thr Ile Thr Asn Asp Lys Gly Arg Leu Ser Lys Glu Asp Ile			
	500	505	510
Glu Lys Met Val Ala Glu Ala Glu Lys Phe Lys Glu Glu Asp Glu Lys			
	515	520	525

Glu Ser Gln Arg Ile Ala Ser Lys Asn Gln Leu Glu Ser Ile Ala Tyr
530 535 540

Ser Leu Lys Asn Thr Ile Ser Glu Ala Gly Asp Lys Leu Glu Gln Ala
545 550 555 560

Asp Lys Asp Thr Val Thr Lys Lys Ala Glu Glu Thr Ile Ser Trp Leu
565 570 575

Asp Ser Asn Thr Thr Ala Ser Lys Glu Glu Phe Asp Asp Lys Leu Lys
580 585 590

Glu Leu Gln Asp Ile Ala Asn Pro Ile Met Ser Lys Leu Tyr Gln Ala
595 600 605

Gly Gly Ala Pro Gly Gly Ala Ala Gly Gly Ala Pro Gly Gly Phe Pro
610 615 620

Gly Gly Ala Pro Pro Ala Pro Glu Ala Glu Gly Pro Thr Val Glu Glu
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Val Asp

<210> 5
<211> 1929
<212> DNA
<213> *Saccharomyces cerevisiae*

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gctttcactg aactgaaag attgattggt gatgctgcta agaatcaagc tgctatgaat 180
ccttcgaata cgtttttcga cgctaagcgt ttgatcggta gaaacttcaa cgaccagaa 240
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gaattcaaga gaaagaacaa gaaggacttg tctaccaacc aaagagcttt gagaagatta	780
agaaccgctt gtgaaagagc caagagaact ttgtcttctt ccgctcaaac ttccgttgaa	840
attgactctt tgttcgaagg tatcgatttc tacacttcca tcaccagagc cagattcgaa	900
gaattgtgtg ctgacttggt cagatctact ttggaccagc ttgaaaaggc cttgagagat	960
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